REMARKS

Applicant notes that the election of the Claims in Group I (Claims 1, 4-9, and 13-17) made in the Response dated April 20, 2001, has been recorded. Thus, Claims 1, 4-9, and 13-17 were pending in the present application. Applicant added dependent Claims 18-21 in the Response faxed May 15, 2002. The Examiner has withdrawn Claims 2, 3 and 10-12, as being directed to a non-elected Group. In the present Response, Claims 16-19 have been cancelled without prejudice and new Claims 22 and 23 have been added. These new Claims are directed toward the CP1 nucleic acid and amino acid sequences. As these Claims find more than sufficient support in the Specification, these Claims do not contain new matter. Thus, Claims 1, 4-9, and 13-15, 20-23 are currently pending.

Applicant note that the Examiner has indicated that some references included in the PTO-1449 form have not been entered into this case. As these references were included solely to show the state of the art in general, Applicant is not submitting these references for the Examiner to enter into the record. As the Examiner is likely well-aware, these references provide techniques and other general information known to those in the art.

While the Examiner has removed multiple objections, one objection to the recitation of "wpr protease" in Claims 15, 17 and 21, has been maintained. The "wpr" abbreviation refers to "cell wall associated" protease. Applicant submits that the wpr protease referred to in the present Specification is the same as the "wprA" enzyme described in Margot *et al.* (Margot *et al.*, Microbiol. 142:3437-3444). Thus, Applicant submits that the terminology in the Claims is definite.

The Examiner has also objected to Claim 13 as being grammatically incorrect. Applicant appreciates the Examiner's suggestion and have amended the Claim to correct the grammar in the Claim. The Examiners rejections of the Claims are addressed in the order below:

1) Claims 20 and 21 stand rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite;

2) Claims 16-19 stand rejected under 35 U.S.C. §112, first paragraph, as allegedly not meeting the written description requirement;

3) Claims 1, 4-9, and 13-21 remain rejected under 35 U.S.C. §112, first paragraph as allegedly not meeting the enablement requirement; and

4) Claims 1, 4-9, and 13-21 remain rejected under 35 U.S.C. §102(b) as allegedly being anticipated by WO89/10976;

1) The Claims Are Definite

The Examiner has rejected Claims 20 and 21 under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. Applicant has amended the Claims without prejudice in order to more clearly indicate that SEQ ID NO:1 corresponds to the gene encoding cysteine protease 1 (SEQ ID NO:2). Applicant believes that the Claims are in condition for allowance and respectfully request that this rejection be withdrawn.

2) The Present Specification and Claims Meet the Written Description Requirement

The Examiner has maintained his rejection of Claims 16-19 under 35 U.S.C. §112, first paragraph, as allegedly not meeting the written description requirement. While Applicant must respectfully disagree, in order to further the prosecution of the present application and Applicant's business interests, yet without acquiescing to the Examiner's arguments, Applicant has cancelled Claims 16-19. Applicant reserves the right to pursue these Claims in another application. As these Claims have been cancelled, this rejection is moot and Applicant respectfully requests that this rejection be withdrawn.

3) The Present Specification and Claims Meet the Enablement Requirement

The Examiner has maintained his rejection of Claims 1, 4-9, and 13-21 under 35 U.S.C. §112, first paragraph, as allegedly not meeting the written description requirement. More particularly, the Examiner argues that the Specification does not

support the broad scope of the Claims. The Examiner argues that the Specification does not establish:

A) regarding claims 16 and 17, the sequences of CP1 polypeptides or encoding polypeptides of all gram positive microorganisms, guidance for isolating said sequences from all gram-positive microorganisms, or the predictability that a CP1 gene is present in all gram-positive microorganisms;

B) regions of a CP1 from any gram-positive microorganism, the polypeptide of SEQ ID NO:2, or the polynucleotide of SEQ ID NO:1 that may be mutated with an expectation of obtaining the desired biological activity;

C) regions apr, npr, epr, wpr and mpr from all gram-positive microorganisms or *Bacillus* hosts that may be mutated with an expectation of obtaining the desired biological activity;

D) the predictability that all gram-positive microorganisms or Bacillus hosts will possess a gene encoding SEQ ID NO:2 or the polynucleotide of SEQ ID NO:1 as an undue amount of experimentation would be required to examine all gram-positive microorganisms for the presence of a gene encoding SEQ ID NO:2 or the polynucleotide of SEQ ID NO:1; and

E) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Applicant must respectfully disagree with the Examiner's arguments. With regard to argument A), Applicant submits that the CP1 polypeptide sequences and nucleic acid sequences encoding CP1 polypeptide are indeed disclosed in the Specification as SEQ ID NO:2 and SEQ ID NO:1. Applicant further submits that there is no requirement that Applicant provide predictability as to whether all gram-positive microorganisms contain CP1. The Claims are only directed towards those microorganisms that DO contain CP1. Nonetheless, as indicated above, Claims 16 and 17 have been deleted without prejudice. Therefore, this rejection is moot as to these Claims.

In regard to arguments B and C), Applicant submits that *any* mutation or deletion that results in the inactivation of CP1 proteolytic activity alone, or in combination with mutations or deletions in apr, npr, epr, wpr, and/or mpr is intended. Applicant is not required to provide each and every mutation or deletion that would result in inactivation.

The Specification as filed provides means to identify CP1, as well as the nucleic acid and amino acid sequences of CP1, and means to assess proteolytic activity (*See*, pages 5-9 and 12). The additional proteins are known in the art (*See e.g.*,page 9).

In regard to D), Applicant submits that there is no requirement that Applicant show the predictability that all gram-positive microorganisms or *Bacillus* hosts will possess a gene encoding SEQ ID NO:2 or the polynucleotide of SEQ ID NO:1. Applicant respectfully submits that no undue amount of experimentation would be required to examine gram-positive microorganisms of interest for the nucleic acid sequence of SEQ ID NO:1, or the amino acid sequence of SEQ ID NO:2. Indeed, the present Specification provides means to determine the homology between the CP-1 of SEQ ID NO:1 and other sequences (*See e.g.*, page 12). Furthermore, the amino acid sequence of SEQ ID NO:2 would be relatively easy to compare with other proteases.

In regard to E), Applicant is unsure as to what the Examiner is referring to in the clause "which of the essentially infinite possible choices is likely to be successful." Thus, Applicant cannot address this argument.

Nonetheless, in order to further the prosecution of the present application and Applicant's business interests, yet without acquiescing to the Examiner's arguments, Applicant has amended Claims 1, 13, and 14, and cancelled Claims 4 and 5. With regard to Claim 13, Applicant submits that the *Bacillus* host cell may be any species of *Bacillus*, as this Claim is directed toward transformed cells. Support for these amendments is provided throughout the Specification and no new matter has been added. Applicant reserves the right to pursue the originally filed, similar and/or broader Claims in another application(s). Applicant respectfully submits that the pending Claims are in condition for allowance and request that this rejection be withdrawn.

3) The Claims are Novel

The Examiner has maintained his rejection of Claims 1, 4-9, and 13-17, under 35 U.S.C. §102(b) as being allegedly anticipated by WO 89/10976. The Examiner argues that "applicants have provided no evidence to distinguish CP1 or the polypeptide of SEQ ID NO:2 encoded by SEQ ID NO:2 from the cysteine protease of WO89/10976 nor have applicants distinguished the cysteine protease-deficient AP^-/NP^- B. subtilis mutant of WO89/10976 from the claimed microorganisms . . . While applicants have amended independent claims 1, 13, 18, and 20 to recite the limitation of SEQ ID NO:2 or SEQ ID

NO:1, this limitation does not distinguish the claimed microorganisms and methods of use thereof from the cited prior art as the cysteine protease-deficient AP⁻/NP⁻ B. subtilis of the prior art would inherently have a mutated sequence of SEQ ID NO:1 due to homologous recombination resulting in inactivation of cysteine protease activity." (Office Action, pages 7-8). Applicant must respectfully disagree.

WO 89/10976 teaches a *B. subtilis* strain that is deficient in **both** alkaline protease and neutral protease, as well as a sulfhydryl-dependent *residual* cysteine protease and/or a *residual* serine protease activities. These residual proteases are described as providing residual protease activity in *Bacillus* strains that are apr⁻/npr⁻, and are responsible for the degradation of proteins in cultures of *B. subtilis*.

As previously indicated, there is no teaching in WO 89/10976 of an organism with a mutation or deletion of part or all of the gene encoding CP-1. Indeed, there is no sequence information provided in this publication for any cysteine protease. Applicant submits that the Examiner has provided no evidence that what is described in WO89/10976 is the same as the sequence set forth in SEQ ID NOS: 1 or 2. Indeed, since there are no sequences of any cysteine protease disclosed in WO89/10976, there is no evidence that can support the Examiner's argument. A search of Genbank for each of the inventors named on WO89/10976 failed to identify any sequence information submitted by any of the named inventors regarding a cysteine protease from *B. subtilis*. Furthermore, a search of the Merops database provided numerous cysteine proteases from *B. subtilis*, any of which could conceivably be the same as the WO89/10976 putative cysteine protease. A copy of this printout is attached hereto.

Applicant respectfully submits that:

> "[t]he fact that a certain result or characteristic may occur or be present in the prior art is not sufficient to establish the inherency of that result or characteristic. *In re Rijckaert*, 9 F.3d 1531, 1534, 28 USPQ2d 1955, 1957 (Fed. Cir. 1993)." (MPEP 2122, *emphasis original*).

Furthermore, Applicant respectfully submits:

> "'[t]o establish inherency, the extrinsic evidence 'must make clear that the missing descriptive matter is necessarily present in the thing described in the reference, and that would be so recognized by persons of ordinary skill. Inherency, however, may not be established by probabilities or possibilities. The mere fact that a certain thing may result from a given set of circumstances is not

sufficient." *In re Robertson*, 169 F.3d 743, 745, 49 USPQ2nd 1949, 1950-151 (Fed. Cir. 1999)." (MPEP 2112).

Thus, Applicant respectfully submits that there is simply no teaching nor suggestion in WO 89/10976 of the CP1 of the presently claimed invention. Likewise, there is no teaching in WO 89/10976 of an organism with such a mutation or deletion in CP-1, as well as mutation(s) and/or deletion(s) in at least one of the genes encoding apr, npr, epr, wpr, and/or mpr. Thus, WO 89/10976 does not teach each and every element of the Claims[1], a requirement for a reference to be anticipatory. Nonetheless, in order to further the prosecution of the present application and Applicant's business interests, yet without acquiescing to the Examiner's arguments, the independent Claims have been amended to recite SEQ ID NO:2. Applicant reserves the right to pursue the originally filed and/or broader Claims in other application(s). Applicant respectfully requests that this rejection be withdrawn and the Claims passed to allowance.

CONCLUSION

All grounds of rejection and objection of the Office Action of January 22, 2002, having been addressed, reconsideration of the application is respectfully requested. Should the Examiner believe that a telephone interview would aid in the prosecution of this application, Applicant encourages the Examiner to call the undersigned.

Respectfully submitted,

Dated: September 30, 2002

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[1] "Anticipation is established only when a single prior art reference discloses, expressly or under principles of inherency, each and every element of a claimed invention." *RCA Corp. v. Applied Digital Data Sys., Inc.*, 730 F.2d 1440, 221 USPQ 385, 388 (Fed. Cir. 1984).

APPENDIX I
MARKED-UP VERSION OF SPECIFICATION'S REPLACEMENT PARAGRAPHS AND REWRITTEN, ADDED, AND/OR CANCELLED CLAIMS

The following is a marked-up version of the Specification's replacement paragraphs pursuant to 37 C.F.R. §1.121(b), as well as a marked-up version of the Claims pursuant to 37 C.F.R. §1.121 (c)(1)(ii) with instructions and markings showing changes made herein to the previous version of record of the specification and claims. Underlining denotes added text while bracketing denotes deleted text.

IN THE CLAIMS:

Please cancel Claims 4, 5, and 16-19.

Please amend the Claims as follows:

1. (Twice Amended) A [gram-positive microorganism] <u>*Bacillus subtilis*</u> having a mutation or deletion of part or all of the gene encoding cysteine protease-1 CP1, wherein said gene encodes the amino acid sequence set forth in SEQ ID NO:2, and said mutation or deletion results in the inactivation of the CP1 proteolytic activity.

13. (Thrice Amended) A method for the production of a heterologous protein in a <u>transformed</u> *Bacillus* host cell comprising the steps of:

(c) obtaining a *Bacillus* host cell comprising <u>a</u> nucleic acid encoding said heterologous protein wherein said host cell contains a mutation or deletion in at least one of the genes encoding *B. subtilis* cysteine protease 1, wherein said at least one of the genes encoding cysteine protease 1 encodes the amino acid sequence set forth in SEQ ID NO:2; and

(d) growing said *Bacillus* host cell under conditions suitable for the expression of said heterologous protein.

14. (Twice Amended) The method of Claim 13 wherein said *Bacillus* <u>host</u> cell is selected from the group consisting of *Bacillus subtilis*, *B. licheniformis*, *B. lentus*, *B. brevis*, *B. stearothermophilus*, *B. alkalophilus*, *B. amyloliquefaciens*, *B. coagulans*, *B. circulans*, *B. lautus*, and *B. thuringiensis*.

20. (Amended) The method of Claim 13, wherein said [*Bacillus*, comprises the nucleic acid sequence set forth in SEQ ID NO:1] at least one of the genes encoding cysteine protease 1 comprises the nucleic acid sequence set forth in SEQ ID NO:1.

Please add the following new Claims:

22. A *Bacillus subtilis* cysteine protease-1 encoded by a nucleic acid sequence comprising SEQ ID NO:1.

23. A *Bacillus subtilis* cysteine protease-1 set forth in an amino acid sequence comprising SEQ ID NO:2.

Bacillus subtilis

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TAXONOMY	
Taxonomy database identifier: 1423	
Superkingdom	Bacteria
Kingdom	Eubacteria
Phylum	Firmicutes
Order	Bacillales
Family	Bacillaceae

PEPTIDASES

Count of known peptidases and homologues: 120

Clan	Family	Code	Peptidase or homologue (subtype)	Gene	Link	Locus
AC	A8	A08.001	signal peptidase II	lspA/lsp	BG11793	
AD	A24	A24 unassigned	family A24 unassigned peptidase (ComC protein)	comC	BG10323	
CA	C39	C39 unassigned	family C39 unassigned peptidase (sunT protein)	sunT	BG12683	
CF	C15	C15.001	pyroglutamyl peptidase I (prokaryote)	pcp	BG10873	
CJ	C56	C56 unassigned	family C56 unassigned peptidase (GSP18 N-terminal fragment)	yfkM	BG12929	
		C56 unassigned	family C56 unassigned peptidase (YraA protein)	yraA	BG13776	
CX	C40	C40.002	murein endopeptidase lytF (*Bacillus subtilis*) (YhdD protein)	yhdD/lytF	BG13010	
		C40.003	lytE g.p. (*Bacillus subtilis*) (PapQ protein)	LytE/papQ	BG11406	
		C40 unassigned	family C40 unassigned peptidase (YwtD protein)	ywtD	BG12535	
		C40 unassigned	family C40 unassigned peptidase (YddH protein)	yddH	BG12115	
		C40 unassigned	family C40 unassigned peptidase (YkfC protein)	ykfC	BG13233	
		C40 unassigned	family C40 unassigned peptidase (YojL protein)	yojL	BG13564	
MA(E)	M3B	M03.007	oligopeptidase F (YjbG protein)	yjbG	BG13136	
		M3 unassigned	subfamily M3B unassigned peptidase (YusX protein)	yusX	BG14036	
	M4	M04.012	neutral protease B (*Bacillus subtilis*)	nprB	BG10691	
		M04.014	bacillolysin	nprE	BG10448	
	M32	M32 unassigned	family M32 unassigned peptidase (YpwA protein)	ypwA	BG11458	
	M41	M41.009	FtsH-2 protease	ftsH	BG10132	

MC	M14C	M14.008	gamma-D-glutamyl-(L)-meso-diaminopimelate peptidase I (*Bacillus* sp.)	yqgT	BG11687	
MD	M15B	M15.011	VanX D-Ala-D-Ala dipeptidase	yodJ	BG13538	
	M15C	M15.020	ply endolysin	ycdD	BG12760	
ME	M16B	M16 unassigned	subfamily M16B unassigned peptidase (YmxG protein)	ymxG	BG10779	
	M16C	M16 unassigned	subfamily M16C unassigned peptidase (YmfH protein)	ymfH	BG13428	
	M16X	M16 unassigned	family M16 unassigned peptidase (YwhN protein)	albF/ywhN	BG12466	
MF	M17	M17 unassigned	family M17 unassigned peptidase (YuiE protein)	yuiE/pepA	BG13970	
MG	M24A	M24.001	methionyl aminopeptidase type 1	map	BG10447	
		M24.001	methionyl aminopeptidase type 1 (YflG protein)	yflG	BG12942	
	M24B	M24.006	Memame-AA019 peptidase	ykvY	BG13326	
		M24 unassigned	subfamily M24B unassigned peptidase (YqhT protein)	yqhT	BG11708	
MH	M20A	M20 non-peptidase homologue	subfamily M20A non-peptidase homologue (acetylornithine deacetylase)	argE/yokP	BG10192	
		M20 unassigned	subfamily M20A unassigned peptidase (YqjE protein)	yqjE	BG11734	
		M20 unassigned	subfamily M20A unassigned peptidase (YtjP protein)	ytjP	BG13867	
		M20 unassigned	subfamily M20A unassigned peptidase (RocB protein)	rocB	BG10623	
		M20 unassigned	subfamily M20A unassigned peptidase (YlmB protein)	ylmB	BG13371	
	M20B	M20.003	peptidase T	pepT	BG11842	
	M28A	M28 unassigned	subfamily M28A unassigned peptidase (YwaD protein)	ywaD/ipa-8r	BG10554	
	M40	M40 non-peptidase homologue	family M40 non-peptidase homologue (amidohydrolase AMHX)	amhX	BG11789	
		M40 non-peptidase homologue	family M40 non-peptidase homologue (hippuricase)	hipO/ytnL	BG12596	
		M40 non-peptidase homologue	family M40 non-peptidase homologue (yurH protein)	yurH	BG13994	
		M40 unassigned	family M40 unassigned peptidase (YhaA protein)	yhaA	BG12982	
		M40 unassigned	family M40 unassigned peptidase (yxeP protein)	yxeP/lp9H	BG11892	
		M40 unassigned	family M40 unassigned peptidase (YkuR protein)	ykuR	BG13302	
	M42	M42 unassigned	family M42 unassigned peptidase (YtoP protein)	ytoP	BG13898	

		M42 unassigned	family M42 unassigned peptidase (YsdC protein)	ysdC/yscD	BG12317	
MJ	M38	Non-peptidase homologue M38.972	dihydro-orotase (dihydroorotase)	pyrC	BG10714	
		M38 non-peptidase homologue	family M38 non-peptidase homologue (urease alpha subunit)	ureC	BG11983	
		M38 non-peptidase homologue	family M38 non-peptidase homologue (YunH protein)	yunH	BG13982	
		M38 non-peptidase homologue	family M38 non-peptidase homologue (adenine deaminase)	adeC/ade	BG11044	
MK	M22	M22 unassigned	family M22 unassigned peptidase (YdiE protein)	ydiE/gcp	BG12202	
		M22 unassigned	family M22 unassigned peptidase (YdiC protein)	ydiC	BG12200	
ML	M63	M63.001	gpr protease	gpr	BG10436	
MM	M50A	M50.004	Mername-AA134 peptidase (YLUC protein)	yluC	BG13410	
	M50B	M50.002	sporulation factor SpoIVFB	spoIVFB	BG10332	
		M50 unassigned	subfamily M50B unassigned peptidase (YwhC protein)	ywhC	BG12457	
MN	M55	M55.001	D-aminopeptidase DppA	dppA/dciAB	BG10842	
MX	M29	M29.002	aminopeptidase II (*Bacillus*-type)	ampS	BG10986	
	M48A	M48.009	YhfN protein (*Bacillus subtilis*) (YhfN protein)	yhfN	BG11029	
	M48B	M48.002	HtpX endopeptidase (YkrL protein)	ykrL/htpX	BG13274	
PA(S)	S1B	S01.272	glutamyl endopeptidase (*Bacillus subtilis*)	mpr	BG10690	
	S1C	S01.273	protease Do (YkdA protein)	htrA/ykdA	BG12608	
		S01.273	protease Do (YycK protein)	ntrC/yycK/yyxA	BG11054	
		S1 unassigned	subfamily S1C unassigned peptidase (YvtB protein)	yvtA/yvtB	BG14155	
	S55	S55.001	SpoIVB peptidase	spoIVB	BG10311	
PB(C)	C44	C44.001	glutamine phosphoribosylpyrophosphate amidotransferase precursor	purF	BG10707	
		Non-peptidase homologue C44.971	glucosamine-fructose-6-phosphate aminotransferase (glucosamine-fructose-6-phosphate aminotransferase)	glmS	BG10948	
PB(T)	T1B	T01.007	CodW component of CodWX peptidase	hslV/codW	BG10966	
	T3	T03.001	gamma-glutamyltransferase 1 (bacterial) (m-type 1)	ggt	BG11838	
			gamma-glutamyltransferase 1			

		T03.001	(bacterial) (m-type 2)			
		T03.014	gamma-glutamyltransferase 2 (bacterial) (YwrD protein)	ywrD	BG12523	
SB	S8A	S08.004	wprA g.p. (*Bacillus* sp.) (WprA protein)	wprA	BG11846	
		S08.017	bacilliopeptidase F	hspN/bpr	BG10233	
		S08.030	Mername-AA055 peptidase	ispA	BG10674	
		S08.036	subtilisin E (I168)	aprE	BG10190	
		S08.037	subtilisin DY (DY)	apr		
		S08.042	subtilisin amylosacchariticus (amylosacchariticus)	aprE/apr/aprA/sprE		
		S8 unassigned	subfamily S8A unassigned peptidase (AprX protein)	aprX	BG12567	
		S8 unassigned	subfamily S8A unassigned peptidase (ParA protein)	parA		
		S8 unassigned	subfamily S8A unassigned peptidase (m-type 1)	sub		
		S8 unassigned	subfamily S8A unassigned peptidase (endopeptidase EPR)	epr	BG10561	
		S8 unassigned	subfamily S8A unassigned peptidase (endopeptidase VPR)	vpr	BG10591	
	S53	S53.004	kumamolysin (*Bacillus* novosp. MN-32)	kumA		
SC	S9C	S9 unassigned	subfamily S9C unassigned peptidase (YuxL protein)	yuxL	BG10463	
	S33	S33 non-peptidase homologue	family S33 non-peptidase homologue (YugF protein)	yugF	BG12360	
		S33 non-peptidase homologue	family S33 non-peptidase homologue (YraK protein)	yraK	BG12275	
		S33 non-peptidase homologue	family S33 non-peptidase homologue (YtxM protein)	ytxM	BG10685	
		S33 unassigned	family S33 unassigned peptidase (YbaC protein)	ybaC	BG13231	
		S33 unassigned	family S33 unassigned peptidase (YisY protein)	yisY	BG13104	
		S33 unassigned	family S33 unassigned peptidase (YclE protein)	yclE	BG12026	
SE	S11	S11.001	D-Ala-D-Ala carboxypeptidase A (DacA protein)	dacA	BG10074	
		S11.005	D-Ala-D-Ala carboxypeptidase DacF (DacF protein)	dacF	BG10295	
		S11 unassigned	family S11 unassigned peptidase (penicillin-binding protein 5*)	dacB	BG10527	
	S12	S12 unassigned	family S12 unassigned peptidase (YbbE protein)	ybbE	BG11566	
		S12	family S12 unassigned			

		unassigned	peptidase (penicillin-binding protein pbpX)	pbpX	BG12642	
		S12 unassigned	family S12 unassigned peptidase (penicillin-binding protein pbpE)	pbpE	BG10390	
	S13	S13.001	D-Ala-D-Ala peptidase C (deduced from nucleotide sequence by MEROPS)			
		S13.002	D-Ala-D-Ala carboxypeptidase (*Actinomadura* strain R39)	pbp	BG10969	
SF	S16	S16.001	lon protease (type 1) (A)	lonA	BG10338	
		S16 unassigned	family S16 unassigned peptidase (YlbL protein)	ylbL	BG13364	
		S16 unassigned	family S16 unassigned peptidase (B)	lonB/lon2	BG11077	
	S24	S24 unassigned	family S24 unassigned peptidase (SOS regulatory protein dinR)	lexA/dinR	BG10678	
	S26A	S26.003	signal peptidase SipS (SipS)	sipS	BG10515	
		S26.004	signal peptidase SipT	sipT	BG11977	
		S26.005	signal peptidase SipU	SipU/YCSB	BG11223	
		S26.006	signal peptidase SipV	sipV/yhjF	BG12674	
		S26.007	signal peptidase SipP	sipP		
		S26.007	signal peptidase SipP (SipP)	sipP/sipP40		
	S26B	S26.011	signal peptidase SipW (*Bacillus* sp.)	sipW/yqhE	BG11696	
SK	S14	S14.001	endopeptidase Clp (type 1)	clpP/lopP/yvdN	BG19016	
		S14 unassigned	family S14 unassigned peptidase (TepA protein)	ymfB/tepA	BG11055	
SM	S41A	S41 unassigned	subfamily S41A unassigned peptidase (YvjB protein)	yvjB	BG14110	
		S41 unassigned	subfamily S41A unassigned peptidase (CtpA protein)	ctpA/yzbD/orfRM1	BG11794	
SX	S49	S49.001	protease IV (YteI protein)	yteI/sppA	BG13839	
	S54	S54 unassigned	family S54 unassigned peptidase (YqgP protein)	yqgP	BG11683	
		S54 unassigned	family S54 unassigned peptidase (YdcA protein)	ydcA	BG13231	
UX	U4	U04.001	sporulation factor SpoIIGA	spoIIGA	BG10234	
	U32	U32 unassigned	family U32 unassigned peptidase (YrrN protein)	yrrN	BG13795	
		U32 unassigned	family U32 unassigned peptidase (YrrO protein)	yrrO	BG13796	
	U57	U57.001	yabG protein (*Bacillus* sp.)	yabG	BG10106	
	U61	U61 unassigned	family U61 unassigned peptidase (YocD protein)	yocD	BG13517	
		U61 unassigned	family U61 unassigned peptidase (YkfA protein)	YkfA	BG13231	

Peptidases of Bacillus subtilis